SCORE Search Results Details for Application 09961086 and Search Result 20080917_142908_us-09-961-086a-1.rag.

This page gives you Search Results detail for the Application 09961086 and Search Result 20080917_142908_us-09-961-086a-1.rag.

Go Back to previous page

GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: September 18, 2008, 21:55:52 ; Search time 231 Seconds
(without alignments)
2130.276 Million cell updates/sec

Title: US-09-961-086A-1
Perfect score: 3352
Sequence: 1 MSSSNVEVFIPVSQGNTNGF.....MIVIFLTIAYLKLLFLKKYS 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4151667 seqs, 751288301 residues

Total number of hits satisfying chosen parameters: 4151667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200808:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

9: geneseqp2004b:*
10: geneseqp2005:*
11: geneseqp2006:*
12: geneseqp2007:*
13: geneseqp2008:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3352	100.0	655	5	AAU80029	Aau80029 Human ABC
2	3352	100.0	663	2	AAY15221	Aay15221 Breast Ca
3	3346	99.8	655	4	AAB60104	Aab60104 Human tra
4	3346	99.8	655	5	AAO14781	Aao14781 Human BCR
5	3346	99.8	655	5	AAU80028	Aau80028 Human ABC
6	3346	99.8	655	6	ADA10917	Ada10917 Human cDN
7	3346	99.8	655	6	ABR58077	Abr58077 Human ABC
8	3346	99.8	655	7	ADC54182	Adc54182 Human bre
9	3346	99.8	655	7	ADG38394	Adg38394 Human wil
10	3346	99.8	655	8	ADK67372	Adk67372 Human wil
11	3346	99.8	655	8	ADI57316	Adi57316 ATP-bindi
12	3346	99.8	655	8	ADI57315	Adi57315 ATP-bindi
13	3346	99.8	655	8	ADI57243	Adi57243 Human ATP
14	3346	99.8	655	8	ADI57311	Adi57311 ATP-bindi
15	3346	99.8	655	10	ALR79140	Alr79140 Vascular
16	3346	99.8	655	10	ALR79139	Alr79139 Vascular
17	3346	99.8	655	11	AEG21952	Aeg21952 Human BCR
18	3346	99.8	655	11	AEJ15196	Aej15196 Human BCR
19	3346	99.8	655	13	ARL93258	Arl93258 Human BCR
20	3345	99.8	655	8	ADI57314	Adi57314 ATP-bindi
21	3343	99.7	655	7	ADG38390	Adg38390 Human BCR
22	3343	99.7	655	8	ADI57310	Adi57310 ATP-bindi
23	3342	99.7	655	7	ADG38388	Adg38388 Human BCR
24	3342	99.7	655	11	AEJ15198	Aej15198 Human BCR
25	3340	99.6	655	8	ADI57312	Adi57312 ATP-bindi
26	3339	99.6	665	5	AAO14783	Aao14783 Human BCR
27	3338	99.6	655	5	ABB07273	Abb07273 Human BCR
28	3338	99.6	655	8	ADI57313	Adi57313 ATP-bindi
29	3331	99.4	655	3	AAY95365	Aay95365 ATP-bindi
30	3331	99.4	655	4	AAU04348	Aau04348 Human BCR
31	3331	99.4	655	5	ABB07270	Abb07270 Human BCR
32	3331	99.4	655	5	ABP52127	Abp52127 Homo sapi
33	3331	99.4	655	7	ABU63376	Abu63376 Human mit
34	3331	99.4	655	10	AEB87761	Aeb87761 Human BCR

35	3331	99.4	655	11	AEE72329	Aee72329 Human tar
36	3331	99.4	655	11	AEJ15197	Aej15197 Human BCR
37	3331	99.4	665	5	AAO14782	Aao14782 Human BCR
38	3225	96.2	655	11	AEJ15192	Aej15192 Rhesus mo
39	3223.5	96.2	654	11	AEJ15195	Aej15195 Rhesus mo
40	3053.5	91.1	604	2	AAW73627	Aaw73627 Human sec
41	3053.5	91.1	604	5	ABP61858	Abp61858 Human pol
42	2927	87.3	623	8	ADJ27182	Adj27182 Human TRI
43	2862	85.4	658	12	AEN69489	Aen69489 Bovine AB
44	2757	82.2	657	5	ABB07272	Abb07272 Murine BC
45	2325	69.4	456	4	AAB93564	Aab93564 Human pro

ALIGNMENTS

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RESULT 1
AAU80029
ID   AAU80029 standard; protein; 655 AA.
XX
AC   AAU80029;
XX
DT   15-JUN-2007  (revised)
DT   15-JUL-2002  (first entry)
XX
DE   Human ABCG2 mutant 482T.
XX
KW   Human; ABCG2; transporter protein; anticancer drug tolerance;
KW   indocarbazole; mutant; mutein; BOND_PC; breast cancer resistance protein;
KW   breast cancer resistance protein [Homo sapiens]; GO166; GO5215; GO5524;
KW   GO6810; GO8559; GO9315; GO16020; GO16021; GO16887; GO42493.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 482
FT                   /note= "Wild type Arg substituted by Thr"
XX
PN   WO200228894-A1.
XX
PD   11-APR-2002.
XX
PF   18-SEP-2001; 2001WO-JP008112.
XX
PR   03-OCT-2000; 2000JP-00303441.
XX
PA   (BANY ) BANYU PHARM CO LTD.
XX
```

PI Komatani H, Hara Y, Kotani H, Nakagawa R;
XX
DR WPI; 2002-352228/38.
DR N-PSDB; ABK49911.
DR PC:NCBI; gi4038352.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT ABCG2 gene encoding transporter protein capable of selectively
PT transporting indocarbazole compounds, useful in screening inhibitors and
PT anticancer agents for administration in chemotherapy.
XX
PS Disclosure; Page 87-90; 98pp; Japanese.
XX
CC The invention relates to an ABCG2 gene encoding a transporter protein
CC capable of imparting tolerance to an anticancer agent in mammals
CC comprising a fully defined sequence as given in the specification or an
CC amino acid sequence based on the sequence but with some amino acids
CC substituted, deleted or added. The gene and encoded protein are useful in
CC screening inhibitors and anticancer agents for administration in
CC chemotherapy with enhancement in sensitivity of cancer cell tolerance.
CC The gene relating to drug tolerance can be modified e.g. with the
CC transporter inhibitors, screened compounds, antibodies and antisense
CC nucleotides. The transporter is capable of selectively transporting
CC indocarbazole compounds extracellularly. The present sequence represents
CC the amino acid sequence of human ABCG2 mutant 482T
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 100.0%; Score 3352; DB 5; Length 655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
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Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655


RESULT 2
AAY15221
ID   AAY15221 standard; protein; 663 AA.
XX
AC   AAY15221;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Breast Cancer Resistance Protein (BCRP).
XX
KW   breast cancer; drug resistance; ATP-binding cassette; ABC;
KW   xenobiotic transporter; chemotherapy; mitoxantrone; doxorubicin;
KW   breast cancer resistance protein; BCRP.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          87. .95
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```
FT                   /note= "Walker A motif"
FT   Domain          221. .236
FT                   /note= "Phosphopantetheine site"
FT   Modified-site   345. .347
FT                   /note= "Glycosylation site on N"
FT   Region          405. .422
FT                   /label= TM1
FT                   /note= "Transmembrane region"
FT   Modified-site   425. .427
FT                   /note= "Glycosylation site on N"
FT   Region          546. .563
FT                   /label= TM2
FT   Modified-site   564. .566
FT                   /note= "Glycosylation site on N"
FT   Modified-site   604. .606
FT                   /note= "Glycosylation site on N"
FT   Region          638. .655
FT                   /label= TM3
XX
PN   WO9940110-A1.
XX
PD   12-AUG-1999.
XX
PF   05-FEB-1999;   99WO-US002577.
XX
PR   05-FEB-1998;   98US-0073763P.
XX
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI   Ross DD,  Doyle LA,  Abruzzo L;
XX
DR   WPI; 1999-494273/41.
DR   N-PSDB; AAZ06360.
XX
PT   New breast cancer resistance protein useful for production of antibodies
PT   to inhibit resistance activity for enhancing chemotherapy treatment.
XX
PS   Claim 4; Fig 2a; 80pp; English.
XX
CC   The Breast Cancer Resistance Protein (BCRP) is an ATP-binding cassette
CC   (ABC) transporter protein. It has a molecular mass of approximately 72.3
CC   kilodaltons (kD) exclusive of any glycosylation. Expression of BCRP in
CC   drug sensitive human cancer cells confers resistance to mitoxantrone,
CC   doxorubicin, and daunorubicin, and reduces daunorubicin accumulation in
CC   the cloned transfected cells. The protein is useful for producing
CC   antibodies and antisense probes, which can be used to inhibit the
CC   activity of BCRP, therefore enhancing a cancer patient's chemotherapy
CC   treatment. The antibodies and probes overcomes the problems of breast
CC   cancer resistance proteins to make chemotherapy treatment more effective
```

XX
SQ Sequence 663 AA;

Query Match 100.0%; Score 3352; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
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Db          9 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 68

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 128

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 188

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 248

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 308

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 368

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 428

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 488

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
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Db        489 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 548

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 608

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        609 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 663


RESULT 3
AAB60104
ID   AAB60104 standard; protein; 655 AA.
XX
AC   AAB60104;
XX
DT   15-JUN-2007  (revised)
DT   28-MAR-2001  (first entry)
XX
DE   Human transport protein TPPT-24.
XX
KW   Human; transport protein; TPPT; transport disorder; metabolic disorder;
KW   neurological disorder; cardiovascular disorder; reproductive disorder;
KW   immune disorder; cancer; BOND_PC;
KW   ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW   ATP-binding cassette, sub-family G (WHITE), member 2;
KW   ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW   ATP-binding cassette superfamily G (White) member 2;
KW   ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW   Breast Cancer Resistance Protein;
KW   Breast Cancer Resistance Protein [Homo sapiens];
KW   ATP-binding cassette sub-family G member 2;
KW   ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW   GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW   GO9315.
XX
OS   Homo sapiens.
XX
PN   WO200078953-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US016668.
XX
PR   17-JUN-1999;   99US-0139923P.
PR   10-AUG-1999;   99US-0148177P.
PR   18-AUG-1999;   99US-0149357P.
PR   28-OCT-1999;   99US-0162287P.
```

XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yang J, Yue H, Hillman JL, Tang YT, Bandman O, Burford N;
PI Baughn MR, Azimzai Y, Lu DAM, Au-Young J, Patterson C;
XX
DR WPI; 2001-041424/05.
DR N-PSDB; AAF27724.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Isolated polypeptide with a human transport protein sequence is useful
PT for the diagnosis, prevention and treatment of disorders associated with
PT the immune, reproductive and cardiovascular systems.
XX
PS Claim 2; Page 126-127; 165pp; English.
XX
CC The present invention provides the protein and coding sequences for 43
CC novel human transport proteins (designated TPPTs). These can be used in
CC the diagnosis and treatment of transport, metabolic, neurological,
CC reproductive, cardiovascular and immune disorders, and cell proliferative
CC disorders such as cancer
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 4; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
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Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
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Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
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Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
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Db         301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy         361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
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Db         361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy         421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
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Qy         481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
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Db         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
```

```
RESULT 4
AAO14781
ID   AAO14781 standard; protein; 655 AA.
XX
AC   AAO14781;
XX
DT   15-JUN-2007  (revised)
DT   28-JUN-2002  (first entry)
XX
DE   Human BCRP protein.
XX
KW   Human; BCRP protein; membrane penetrating region; cancer; BOND_PC;
KW   ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
```

KW ATP-binding cassette, sub-family G (WHITE), member 2;
KW ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW ATP-binding cassette superfamily G (White) member 2;
KW ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW Breast Cancer Resistance Protein;
KW Breast Cancer Resistance Protein [Homo sapiens];
KW ATP-binding cassette sub-family G member 2;
KW ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW GO9315.
XX
OS Homo sapiens.
XX
PN JP2002065277-A.
XX
PD 05-MAR-2002.
XX
PF 31-AUG-2000; 2000JP-00263742.
XX
PR 31-AUG-2000; 2000JP-00263742.
XX
PA (GANK-) ZH GAN KENKYUKAI.
XX
DR WPI; 2002-324198/36.
DR N-PSDB; AAL42412.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Mutant BCRP protein useful for treatment of cancer.
XX
PS Claim 13; Page 7-8; 15pp; Japanese.
XX
CC The invention comprises a mutant human BCRP protein, having a deletion,
CC replacement or addition of at least one amino acid in the fifth membrane
CC penetrating region of the wild-type BCRP protein. The mutant BCRP protein
CC can be used for the treatment of cancer. The present amino acid sequence
CC represents a human BCRP protein
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 5; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655


RESULT 5
AAU80028
ID   AAU80028 standard; protein; 655 AA.
XX
AC   AAU80028;
XX
```

DT 15-JUN-2007 (revised)
DT 15-JUL-2002 (first entry)
XX
DE Human ABCG2.
XX
KW Human; ABCG2; transporter protein; anticancer drug tolerance;
KW indocarbazole; BOND_PC; ATP-binding cassette, sub-family G, member 2;
KW breast cancer resistance protein; placenta specific MDR protein;
KW mitoxantrone resistance protein;
KW ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW ATP-binding cassette transporter G2;
KW ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW ATP-binding cassette, sub-family G (WHITE), member 2;
KW ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW ATP-binding cassette superfamily G (White) member 2;
KW ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW Breast Cancer Resistance Protein;
KW Breast Cancer Resistance Protein [Homo sapiens];
KW ATP-binding cassette sub-family G member 2;
KW ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW GO9315.
XX
OS Homo sapiens.
XX
PN WO200228894-A1.
XX
PD 11-APR-2002.
XX
PF 18-SEP-2001; 2001WO-JP008112.
XX
PR 03-OCT-2000; 2000JP-00303441.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Komatani H, Hara Y, Kotani H, Nakagawa R;
XX
DR WPI; 2002-352228/38.
DR N-PSDB; ABK49901.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT ABCG2 gene encoding transporter protein capable of selectively
PT transporting indocarbazole compounds, useful in screening inhibitors and
PT anticancer agents for administration in chemotherapy.
XX

PS Claim 1; Page 71-76; 98pp; Japanese.
XX
CC The invention relates to an ABCG2 gene encoding a transporter protein
CC capable of imparting tolerance to an anticancer agent in mammals
CC comprising a fully defined sequence as given in the specification or an
CC amino acid sequence based on the sequence but with some amino acids
CC substituted, deleted or added. The gene and encoded protein are useful in
CC screening inhibitors and anticancer agents for administration in
CC chemotherapy with enhancement in sensitivity of cancer cell tolerance.
CC The gene relating to drug tolerance can be modified e.g. with the
CC transporter inhibitors, screened compounds, antibodies and antisense
CC nucleotides. The transporter is capable of selectively transporting
CC indocarbazole compounds extracellularly. The present sequence represents
CC the amino acid sequence of human ABCG2 protein
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 5; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy         421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy         481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655


RESULT 6
ADA10917
ID   ADA10917 standard; protein; 655 AA.
XX
AC   ADA10917;
XX
DT   15-JUN-2007  (revised)
DT   06-NOV-2003  (first entry)
XX
DE   Human cDNA differentially expressed in colon cancer #23 product.
XX
KW   differential expression; colon cancer; cancer; human; BOND_PC;
KW   ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW   ATP-binding cassette, sub-family G (WHITE), member 2;
KW   ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW   ATP-binding cassette superfamily G (White) member 2;
KW   ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW   Breast Cancer Resistance Protein;
KW   Breast Cancer Resistance Protein [Homo sapiens];
KW   ATP-binding cassette sub-family G member 2;
KW   ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
```

KW GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW GO9315.
XX
OS Homo sapiens.
XX
PN US2002160382-A1.
XX
PD 31-OCT-2002.
XX
PF 11-OCT-2001; 2001US-00981353.
XX
PR 11-OCT-2000; 2000US-0239841P.
XX
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
XX
PI Lasek AW, Jones DA;
XX
DR WPI; 2003-265756/26.
DR N-PSDB; ADA10916.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT New combination comprising cDNAs that are differentially expressed in
PT colon disorder, useful for diagnosing, treating, staging or monitoring
PT treatment for colon cancers.
XX
PS Example 14; SEQ ID NO 35; 231pp; English.
XX
CC The invention relates to a combination comprising cDNAs that are
CC differentially expressed in colon disorder. The methods and compositions
CC of the present invention are useful for diagnosing, treating, staging or
CC monitoring treatment for colon cancer. They are also useful in high
CC throughput methods for using cDNAs to detect differential expression of
CC nucleic acids in a sample, screening molecules or compounds to identify a
CC ligand which specifically binds a cDNA and using a protein to screen
CC molecules or compounds to identify at least one ligand which specifically
CC binds the protein. The present sequence represents the amino acid
CC sequence of a human cDNA differentially expressed in colon cancer
CC protein.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 6; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
```

RESULT 7
ABR58077
ID   ABR58077 standard; protein; 655 AA.

XX
AC ABR58077;
XX
DT 15-JUN-2007 (revised)
DT 15-OCT-2003 (first entry)
XX
DE Human ABCG2 protein.
XX
KW ABCG2; antidiabetic; cell therapy; diabetes mellitus;
KW pancreatic stem cell; islets of langerhans; insulin; BOND_PC;
KW ATP-binding cassette, sub-family G, member 2;
KW breast cancer resistance protein; placenta specific MDR protein;
KW mitoxantrone resistance protein;
KW ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW ATP-binding cassette transporter G2;
KW ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW ATP-binding cassette, sub-family G (WHITE), member 2;
KW ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW ATP-binding cassette superfamily G (White) member 2;
KW ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW Breast Cancer Resistance Protein;
KW Breast Cancer Resistance Protein [Homo sapiens];
KW ATP-binding cassette sub-family G member 2;
KW ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW GO9315.
XX
OS Homo sapiens.
XX
PN WO2003026584-A2.
XX
PD 03-APR-2003.
XX
PF 26-SEP-2002; 2002WO-US030700.
XX
PR 26-SEP-2001; 2001US-00963875.
PR 11-APR-2002; 2002US-00120687.
PR 02-MAY-2002; 2002US-00136891.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Habener JF, Zulewski H, Thomas MK, Abraham EJ, Vallejo M;
PI Leech CA, Nolan AL, Lechner A;
XX
DR WPI; 2003-354625/33.
DR N-PSDB; ACC80605.

DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Treating a patient with diabetes mellitus by isolating a nestin- or ABCG2
PT -positive pancreatic stem cell from a pancreatic islet of a donor and
PT transferring the stem cell into the patient.
XX
PS Disclosure; Fig 18B; 107pp; English.
XX
CC The invention relates to a method of treating a patient with diabetes
CC mellitus by isolating a nestin- or ABCG2-positive pancreatic stem cell
CC from a pancreatic islet of a donor, and transferring the stem cell into
CC the patient whereby the stem cell differentiates into an insulin-
CC producing cell. Alternatively, the nestin- or ABCG2-positive stem is
CC induced into a pancreatic progenitor cell prior to isolation and
CC transfer. This sequence corresponds to the human ABCG2 protein and the
CC encoding gene is detected in the method of the invention. The method is
CC useful for preparing a pharmaceutical composition for treating diabetes
CC mellitus. The stem cells can be further characterised for correct gene
CC expression using the primers and probes ACC80607-ACC80671
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 6; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
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```
Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
```

```
RESULT 8
ADC54182
ID   ADC54182 standard; protein; 655 AA.
XX
AC   ADC54182;
XX
DT   15-JUN-2007  (revised)
DT   18-DEC-2003  (first entry)
XX
DE   Human breast cancer resistance protein (BCRP) amino acid sequence.
XX
KW   cancer cell; anti-cancer agent; steroid hormone; oestrogenic effect;
KW   BCRP; breast cancer resistance protein; cytostatic; camptothecins;
KW   mitoxantrone; 7-hydroxy staurosporine; adriamycin; cancer chemotherapy;
KW   human; BOND_PC; ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
```

KW ATP-binding cassette, sub-family G (WHITE), member 2;
KW ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW ATP-binding cassette superfamily G (White) member 2;
KW ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW Breast Cancer Resistance Protein;
KW Breast Cancer Resistance Protein [Homo sapiens];
KW ATP-binding cassette sub-family G member 2;
KW ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW GO9315.
XX
OS Homo sapiens.
XX
PN JP2003063989-A.
XX
PD 05-MAR-2003.
XX
PF 23-AUG-2001; 2001JP-00252953.
XX
PR 23-AUG-2001; 2001JP-00252953.
XX
PA (GANK-) ZH GAN KENKYUKAI.
XX
DR WPI; 2003-735321/70.
DR N-PSDB; ADC54181.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Agent that overcomes resistance of cancer cell against anti-cancer agent,
PT comprises a steroid hormone, or a compound which exhibits antagonistic
PT activity against the hormone, with the cancer cell expressing BCRP gene.
XX
PS Example 1; SEQ ID NO 4; 15pp; Japanese.
XX
CC This invention relates to a novel agent which overcomes resistance of a
CC cancer cell against an anti-cancer agent (AA), comprising as an active
CC ingredient a steroid hormone, a compound having oestrogenic effect, or a
CC compound which exhibits antagonistic activity against the hormone, where
CC the cancer cell expresses the BCRP (breast cancer resistance protein)
CC gene. The agent of the invention may have cytostatic activity. The
CC invention is useful for overcoming resistance of a cancer against an anti
CC -cancer agent such as camptothecins, mitoxantrone, 7-hydroxy
CC staurosporine and adriamycin. The therapeutic effective anti-cancer agent
CC is recovered, due to the use of the agent of the invention. Also the
CC dosages of anti-cancer agent can be maintained easily, and adverse
CC effects of cancer chemotherapy can be suppressed. The present sequence is
CC that of the human BCRP protein which was used to develop the novel agent
CC of the invention.
CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 7; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
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Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655


RESULT 9
ADG38394
ID   ADG38394 standard; protein; 655 AA.
XX
AC   ADG38394;
XX
DT   15-JUN-2007  (revised)
DT   26-FEB-2004  (first entry)
XX
DE   Human wild-type BCRP.
XX
KW   Anticancer agent; polymorphism; human; BCRP; cancer cell; BOND_PC;
KW   ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW   ATP-binding cassette, sub-family G (WHITE), member 2;
KW   ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW   ATP-binding cassette superfamily G (White) member 2;
KW   ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW   Breast Cancer Resistance Protein;
KW   Breast Cancer Resistance Protein [Homo sapiens];
KW   ATP-binding cassette sub-family G member 2;
KW   ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW   GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW   GO9315.
XX
OS   Homo sapiens.
XX
PN   JP2003199585-A.
XX
PD   15-JUL-2003.
XX
PF   21-MAY-2002; 2002JP-00145926.
XX
PR   24-OCT-2001; 2001JP-00325883.
XX
PA   (GANK-) ZH GAN KENKYUKAI.
XX
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DR WPI; 2003-819597/77.
DR N-PSDB; ADG38395.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Evaluating sensitivity of test cell to anticancer agent involves
PT identifying gene polymorphism of BCRP.
XX
PS Example 1; SEQ ID NO 7; 18pp; Japanese.
XX
CC The present invention relates to a method for evaluating the sensitivity
CC of a cell to an anticancer agent. The method involves identifying a gene
CC polymorphism in the human BCRP gene (the polymorphism is undefined in the
CC specification). The gene polymorphisms encode variant BCRP polypeptides
CC designated as Q141K, V12M and Q126STOP. Identifying the gene polymorphism
CC of BCRP of a test cell is useful for evaluating the expression grade of
CC the side effect at the time of administering an anticancer agent to the
CC test cell and evaluating the resistance of the test cell to the
CC anticancer agent. BCRP protein is useful in conveying an anticancer agent
CC to cancer cell. The method is efficient in identifying a safer anticancer
CC -agent for treatment. The present sequence represents wild-type BCRP.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 7; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
```

RESULT 10
ADK67372
ID   ADK67372 standard; protein; 655 AA.
XX
AC   ADK67372;
XX
DT   15-JUN-2007 (revised)
DT   18-NOV-2004 (first entry)
XX
DE   Human wild-type ABCG2 (ATP-binding cassette gene) protein.
XX
KW   drug absorption; ABCG2; ATP-binding cassette gene; human; wild-type;
KW   chromosome 4q22; BOND_PC; ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW   ATP-binding cassette, sub-family G (WHITE), member 2;

KW ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW ATP-binding cassette superfamily G (White) member 2;
KW ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW Breast Cancer Resistance Protein;
KW Breast Cancer Resistance Protein [Homo sapiens];
KW ATP-binding cassette sub-family G member 2;
KW ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW GO9315.
XX
OS Homo sapiens.
XX
PN JP2004016042-A.
XX
PD 22-JAN-2004.
XX
PF 13-JUN-2002; 2002JP-00172759.
XX
PR 13-JUN-2002; 2002JP-00172759.
XX
PA (KOKU-) KOKURITSU IYAKUHIN SHOKUHIN EISEI KENKYU.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
XX
DR WPI; 2004-113852/12.
DR N-PSDB; ADK67371.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Novel ABCG2 polynucleotide having a mutation at a specific position,
PT useful for gene diagnosis of abnormality of medicine absorption
PT associated with ABCG2 protein.
XX
PS Claim 1; SEQ ID NO 2; 53pp; Japanese.
XX
CC The invention relates to a novel polynucleotide having a mutation in the
CC codon encoding a glutamine residue present at the 126 position of a 655
CC amino acid sequence. The polynucleotide of the invention may be useful
CC for the estimation or diagnosis of a condition which is associated with
CC abnormal drug absorption and in which the ABCG2 (ATP-binding cassette
CC gene) protein is associated. The current sequence is that of the human
CC wild-type ABCG2 protein of the invention which is encoded by DNA located
CC at chromosome 4q22.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 8; Length 655;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
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RESULT 11

```
ADI57316
ID   ADI57316 standard; protein; 655 AA.
XX
AC   ADI57316;
XX
DT   15-JUN-2007  (revised)
DT   22-APR-2004  (first entry)
XX
DE   ATP-binding cassette transporter ABCG2 D590Y mutant.
XX
KW   drug transport capability; polymorphism; ABCG2; polymorphic mutation;
KW   drug sensitivity; anti-cancer drug; cancer therapy;
KW   cancer cell detection; indolocarbozole compound; human;
KW   ABC transporter superfamily;
KW   ATP-binding cassette transporter superfamily; mutant; mutein; BOND_PC;
KW   ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW   ATP-binding cassette, sub-family G (WHITE), member 2;
KW   ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW   ATP-binding cassette superfamily G (White) member 2;
KW   ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW   Breast Cancer Resistance Protein;
KW   Breast Cancer Resistance Protein [Homo sapiens];
KW   ATP-binding cassette sub-family G member 2;
KW   ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW   GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW   GO9315.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 590
FT                   /note= "Wild type Asp substituted by Tyr"
XX
PN   WO2003107249-A1.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-JP007534.
XX
PR   17-JUN-2002; 2002JP-00175806.
```

XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Kotani H, Mizuarai S;
XX
DR WPI; 2004-156349/15.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Predicting drug transport capability of mammalian cell by collecting
PT sample from mammal, determining polymorphism of nucleotide sequence of
PT ABCG2 gene or polymorphism of amino acid sequence of ABCG2 polypeptide.
XX
PS Example 1; Page; 76pp; English.
XX
CC The invention describes a method of predicting a drug transport
CC capability of a mammalian cell involving collecting a sample from a
CC mammal, determining a polymorphism of the nucleotide sequence of ABCG2
CC gene or a polymorphism of the amino acid sequence of ABCG2 polypeptide.
CC The method is useful for predicting drug transport capability of a
CC mammalian cell. Polynucleotides comprising single nucleotide
CC polymorphisms or polypeptides comprising polymorphic mutations of the
CC ABCG2 protein are useful as diagnostic agent for diagnosing drug
CC sensitivity which involves analyzing a biological sample from a subject
CC and determining the presence or absence of the polynucleotides or
CC polypeptides, where the subject having the polynucleotide and/or the
CC polypeptide is suggested to be sensitive to the indolocarbozole compound.
CC A transformed cell comprising an ABCG2 protein mutant is useful for
CC measuring drug transport capability. By predicting drug transport
CC capability of a mammalian cell, sensitivity of a patient to various drugs
CC such as anti-cancer drugs can be diagnosed and an indicator for the
CC therapy can be obtained. As a result of selecting an anti-cancer drug in
CC cancer therapy and, particularly, detecting a cancer cell(s) which is
CC highly sensitive to indolocarbozole compounds, it is now possible to
CC selectively apply the compounds for the therapy. In addition, the optimum
CC dose of the indolocarbazole compounds in the cancer therapy is found and,
CC at the same time, side effect of the compounds is reduced whereby a
CC highly effective method of using the indolocarbozole compounds is
CC provided. This is the amino acid sequence of a human ABC transporter
CC superfamily (ATP-binding cassette transporter superfamily) protein ABCG2
CC mutant. Note: This sequence does not appear in the specification but has
CC been created using information given in the claims of the invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 8; Length 655;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
```

RESULT 12

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ADI57315
ID   ADI57315 standard; protein; 655 AA.
XX
AC   ADI57315;
XX
DT   15-JUN-2007  (revised)
DT   22-APR-2004  (first entry)
XX
DE   ATP-binding cassette transporter ABCG2 R482T mutant.
XX
KW   drug transport capability; polymorphism; ABCG2; polymorphic mutation;
KW   drug sensitivity; anti-cancer drug; cancer therapy;
KW   cancer cell detection; indolocarbozole compound; human;
KW   ABC transporter superfamily;
KW   ATP-binding cassette transporter superfamily; mutant; mutein; BOND_PC;
KW   ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW   ATP-binding cassette, sub-family G (WHITE), member 2;
KW   ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW   ATP-binding cassette superfamily G (White) member 2;
KW   ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW   Breast Cancer Resistance Protein;
KW   Breast Cancer Resistance Protein [Homo sapiens];
KW   ATP-binding cassette sub-family G member 2;
KW   ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW   GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW   GO9315.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 482
FT                   /note= "Wild type Arg substituted by Thr"
XX
PN   WO2003107249-A1.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-JP007534.
XX
PR   17-JUN-2002; 2002JP-00175806.
```

XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Kotani H, Mizuarai S;
XX
DR WPI; 2004-156349/15.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Predicting drug transport capability of mammalian cell by collecting
PT sample from mammal, determining polymorphism of nucleotide sequence of
PT ABCG2 gene or polymorphism of amino acid sequence of ABCG2 polypeptide.
XX
PS Example 1; Page; 76pp; English.
XX
CC The invention describes a method of predicting a drug transport
CC capability of a mammalian cell involving collecting a sample from a
CC mammal, determining a polymorphism of the nucleotide sequence of ABCG2
CC gene or a polymorphism of the amino acid sequence of ABCG2 polypeptide.
CC The method is useful for predicting drug transport capability of a
CC mammalian cell. Polynucleotides comprising single nucleotide
CC polymorphisms or polypeptides comprising polymorphic mutations of the
CC ABCG2 protein are useful as diagnostic agent for diagnosing drug
CC sensitivity which involves analyzing a biological sample from a subject
CC and determining the presence or absence of the polynucleotides or
CC polypeptides, where the subject having the polynucleotide and/or the
CC polypeptide is suggested to be sensitive to the indolocarbozole compound.
CC A transformed cell comprising an ABCG2 protein mutant is useful for
CC measuring drug transport capability. By predicting drug transport
CC capability of a mammalian cell, sensitivity of a patient to various drugs
CC such as anti-cancer drugs can be diagnosed and an indicator for the
CC therapy can be obtained. As a result of selecting an anti-cancer drug in
CC cancer therapy and, particularly, detecting a cancer cell(s) which is
CC highly sensitive to indolocarbozole compounds, it is now possible to
CC selectively apply the compounds for the therapy. In addition, the optimum
CC dose of the indolocarbazole compounds in the cancer therapy is found and,
CC at the same time, side effect of the compounds is reduced whereby a
CC highly effective method of using the indolocarbozole compounds is
CC provided. This is the amino acid sequence of a human ABC transporter
CC superfamily (ATP-binding cassette transporter superfamily) protein ABCG2
CC mutant. Note: This sequence does not appear in the specification but has
CC been created using information given in the claims of the invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 8; Length 655;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy        481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
```

RESULT 13

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ADI57243
ID   ADI57243 standard; protein; 655 AA.
XX
AC   ADI57243;
XX
DT   15-JUN-2007  (revised)
DT   22-APR-2004  (first entry)
XX
DE   Human ATP-binding cassette transporter ABCG2.
XX
KW   drug transport capability; polymorphism; ABCG2; polymorphic mutation;
KW   drug sensitivity; anti-cancer drug; cancer therapy;
KW   cancer cell detection; indolocarbozole compound; human;
KW   ABC transporter superfamily;
KW   ATP-binding cassette transporter superfamily; BOND_PC;
KW   ATP-binding cassette, sub-family G, member 2;
KW   breast cancer resistance protein; placenta specific MDR protein;
KW   mitoxantrone resistance protein;
KW   ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW   ATP-binding cassette transporter G2;
KW   ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW   MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW   ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW   ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW   ATP-binding cassette, sub-family G (WHITE), member 2;
KW   ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW   ATP-binding cassette superfamily G (White) member 2;
KW   ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW   Breast Cancer Resistance Protein;
KW   Breast Cancer Resistance Protein [Homo sapiens];
KW   ATP-binding cassette sub-family G member 2;
KW   ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW   GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW   GO9315.
XX
OS   Homo sapiens.
XX
PN   WO2003107249-A1.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-JP007534.
XX
PR   17-JUN-2002; 2002JP-00175806.
XX
PA   (BANY ) BANYU PHARM CO LTD.
XX
PI   Kotani H,  Mizuarai S;
XX
```

DR WPI; 2004-156349/15.
DR N-PSDB; ADI57242.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Predicting drug transport capability of mammalian cell by collecting
PT sample from mammal, determining polymorphism of nucleotide sequence of
PT ABCG2 gene or polymorphism of amino acid sequence of ABCG2 polypeptide.
XX
PS Claim 16; SEQ ID NO 2; 76pp; English.
XX
CC The invention describes a method of predicting a drug transport
CC capability of a mammalian cell involving collecting a sample from a
CC mammal, determining a polymorphism of the nucleotide sequence of ABCG2
CC gene or a polymorphism of the amino acid sequence of ABCG2 polypeptide.
CC The method is useful for predicting drug transport capability of a
CC mammalian cell. Polynucleotides comprising single nucleotide
CC polymorphisms or polypeptides comprising polymorphic mutations of the
CC ABCG2 protein are useful as diagnostic agent for diagnosing drug
CC sensitivity which involves analyzing a biological sample from a subject
CC and determining the presence or absence of the polynucleotides or
CC polypeptides, where the subject having the polynucleotide and/or the
CC polypeptide is suggested to be sensitive to the indolocarbozole compound.
CC A transformed cell comprising an ABCG2 protein mutant is useful for
CC measuring drug transport capability. By predicting drug transport
CC capability of a mammalian cell, sensitivity of a patient to various drugs
CC such as anti-cancer drugs can be diagnosed and an indicator for the
CC therapy can be obtained. As a result of selecting an anti-cancer drug in
CC cancer therapy and, particularly, detecting a cancer cell(s) which is
CC highly sensitive to indolocarbozole compounds, it is now possible to
CC selectively apply the compounds for the therapy. In addition, the optimum
CC dose of the indolocarbazole compounds in the cancer therapy is found and,
CC at the same time, side effect of the compounds is reduced whereby a
CC highly effective method of using the indolocarbozole compounds is
CC provided. This is the amino acid sequence of human ABC transporter
CC superfamily (ATP-binding cassette transporter superfamily) protein ABCG2.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 8; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
```

```
Qy          61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy         121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy         181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy         241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300

Qy         301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy         361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy         421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy         481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
               | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
```

RESULT 14
ADI57311
ID   ADI57311 standard; protein; 655 AA.
XX
AC   ADI57311;
XX
DT   15-JUN-2007 (revised)

DT 22-APR-2004 (first entry)
XX
DE ATP-binding cassette transporter ABCG2 Q141K mutant.
XX
KW drug transport capability; polymorphism; ABCG2; polymorphic mutation;
KW drug sensitivity; anti-cancer drug; cancer therapy;
KW cancer cell detection; indolocarbozole compound; human;
KW ABC transporter superfamily;
KW ATP-binding cassette transporter superfamily; mutant; mutein; BOND_PC;
KW ATP-binding cassette, sub-family G, member 2;
KW breast cancer resistance protein; placenta specific MDR protein;
KW mitoxantrone resistance protein;
KW ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW ATP-binding cassette transporter G2;
KW ATP-binding cassette, sub-family G, member 2 [Homo sapiens]; ABCG2; MRX;
KW MXR; ABCP; BCRP; BMDP; MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW ATP-binding cassette sub-family G (WHITE) member 2 [Homo sapiens];
KW ATP-binding cassette, sub-family G (WHITE), member 2;
KW ATP-binding cassette, sub-family G (WHITE), member 2 [Homo sapiens];
KW ATP-binding cassette superfamily G (White) member 2;
KW ATP-binding cassette superfamily G (White) member 2 [Homo sapiens];
KW Breast Cancer Resistance Protein;
KW Breast Cancer Resistance Protein [Homo sapiens];
KW ATP-binding cassette sub-family G member 2;
KW ATP-binding cassette sub-family G member 2 [synthetic construct]; GO166;
KW GO5215; GO5524; GO6810; GO8559; GO16020; GO16021; GO16887; GO42493;
KW GO9315.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 141
FT /note= "Wild type Gln substituted by Lys"
XX
PN WO2003107249-A1.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-JP007534.
XX
PR 17-JUN-2002; 2002JP-00175806.
XX
PA (BANY) BANYU PHARM CO LTD.
XX
PI Kotani H, Mizuarai S;
XX
DR WPI; 2004-156349/15.

DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT Predicting drug transport capability of mammalian cell by collecting
PT sample from mammal, determining polymorphism of nucleotide sequence of
PT ABCG2 gene or polymorphism of amino acid sequence of ABCG2 polypeptide.
XX
PS Claim 6; Page; 76pp; English.
XX
CC The invention describes a method of predicting a drug transport
CC capability of a mammalian cell involving collecting a sample from a
CC mammal, determining a polymorphism of the nucleotide sequence of ABCG2
CC gene or a polymorphism of the amino acid sequence of ABCG2 polypeptide.
CC The method is useful for predicting drug transport capability of a
CC mammalian cell. Polynucleotides comprising single nucleotide
CC polymorphisms or polypeptides comprising polymorphic mutations of the
CC ABCG2 protein are useful as diagnostic agent for diagnosing drug
CC sensitivity which involves analyzing a biological sample from a subject
CC and determining the presence or absence of the polynucleotides or
CC polypeptides, where the subject having the polynucleotide and/or the
CC polypeptide is suggested to be sensitive to the indolocarbozole compound.
CC A transformed cell comprising an ABCG2 protein mutant is useful for
CC measuring drug transport capability. By predicting drug transport
CC capability of a mammalian cell, sensitivity of a patient to various drugs
CC such as anti-cancer drugs can be diagnosed and an indicator for the
CC therapy can be obtained. As a result of selecting an anti-cancer drug in
CC cancer therapy and, particularly, detecting a cancer cell(s) which is
CC highly sensitive to indolocarbozole compounds, it is now possible to
CC selectively apply the compounds for the therapy. In addition, the optimum
CC dose of the indolocarbazole compounds in the cancer therapy is found and,
CC at the same time, side effect of the compounds is reduced whereby a
CC highly effective method of using the indolocarbozole compounds is
CC provided. This is the amino acid sequence of a human ABC transporter
CC superfamily (ATP-binding cassette transporter superfamily) protein ABCG2
CC mutant. Note: This sequence does not appear in the specification but has
CC been created using information given in the claims of the invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 8; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
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Qy          61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
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Db         121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy         181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
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Qy         241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
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Qy         361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420

Qy         421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
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Db         421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

Qy         481 MTMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540
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Qy         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
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Db         541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600

Qy         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
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Db         601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
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RESULT 15
ALR79140
ID   ALR79140 standard; protein; 655 AA.
XX
AC   ALR79140;
XX
DT   28-DEC-2007 (first entry)

XX
DE Vascular disease-associated polypeptide SEQ ID NO:297.
XX
KW diagnosis; stenosis; vasotropic; cardiovascular disease; cardiant;
KW coronary artery disease; heart disease; myocardial infarction;
KW single nucleotide polymorphism; SNP; SNP detection; therapeutic;
KW prophylaxis; BOND_PC; ATP-binding cassette, sub-family G, member 2;
KW breast cancer resistance protein; placenta specific MDR protein;
KW mitoxantrone resistance protein;
KW ATP-binding cassette sub-family G (WHITE) member 2; ABC transporter;
KW ATP-binding cassette transporter G2; ABCG2; MRX; MXR; ABCP; BCRP; BMDP;
KW MXR1; ABC15; BCRP1; EST157481; MGC102821; CDw338;
KW ATP-binding cassette, sub-family G (WHITE), member 2, isoform CRA_a;
KW ATP-binding cassette, sub-family G (WHITE), member 2;
KW ATP-binding cassette superfamily G (White) member 2;
KW ATP-binding cassette sub-family G member 2; GO166; GO5215; GO5524;
KW GO6810; GO8559; GO16020; GO16021; GO16887; GO42493; GO9315.
XX
OS Homo sapiens.
XX
PN WO2005110039-A2.
XX
PD 24-NOV-2005.
XX
PF 09-MAY-2005; 2005WO-US016076.
XX
PR 07-MAY-2004; 2004US-0568845P.
PR 09-NOV-2004; 2004US-0625936P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Luke M;
XX
DR WPI; 2005-811478/82.
DR PC:NCBI; gi62526033.
DR PC:SWISSPROT; Q9UNQ0.
XX
PT New nucleic acid molecule comprising at least 8 contiguous nucleotides,
PT one of which is a single nucleotide polymorphism (SNP), useful in
PT preparing a composition for treating or preventing coronary stenosis.
XX
PS Claim 8; SEQ ID NO 297; 135pp; English.
XX
CC This invention describes a novel nucleic acid comprising at least 8
CC contiguous nucleotides which is used in a method and kit for identifying
CC an individual who has an altered risk for developing coronary stenosis
CC due to the presence of a single nucleotide polymorphism (SNP). The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences SEQ ID NO 1-SEQ ID NO 169 or SEQ ID NO 339-SEQ

CC ID NO 21112, where the presence of the SNP is correlated with an altered
CC risk for coronary stenosis. The detection is carried out by allele-
CC specific probe hybridization, allele-specific primer extension, allele-
CC specific amplification, sequencing, 5' nuclease digestion, molecular
CC beacon assay, oligonucleotide ligation assay, size analysis or single-
CC stranded conformation polymorphism. The nucleic acid molecule is useful
CC in preparing a composition for treating or preventing coronary stenosis
CC e.g. coronary heart disease or myocardial infarction. This sequence
CC represents a polypeptide used in the method of the invention.
CC
CC Revised record issued on 17-DEC-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 655 AA;

Query Match 99.8%; Score 3346; DB 10; Length 655;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSSNVEVFIPVSQGNTNGFPATASNDLKAFTEGAVLSFHNICYRVKLKSGFLPCRKPVE 60

Qy         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEILSNINGIMKPGLNAILGPTGGGKSSLLDVLAARKDPSGLSGDVLINGAPRPANFKCN 120

Qy        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGYVVQDDVVMGTLTVRENLQFSAALRLATTMTNHEKNERINRVIQELGLDKVADSKVGT 180

Qy        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QFIRGVSGGERKRTSIGMELITDPSILFLDEPTTGLDSSTANAVLLLLKRMSKQGRTIIF 240

Qy        241 SIHQPRYSIFKLFDSLTLLASGRLMFHGPAQEALGYFESAGYHCEAYNNPADFFLDIING 300
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Qy        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DSTAVALNREEDFKATEIIEPSKQDKPLIEKLAEIYVNSSFYKETKAELHQLSGGEKKKK 360

Qy        361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480
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Db        421 TGIQNRAGVLFFLTTNQCFSSVSAVELFVVEKKLFIHEYISGYYRVSSYFLGKLLSDLLP 480

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              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 MRMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVAYSASSMALAIAAGQSVVSVATLL 540

Qy        541 MTICFVFMMIFSGLLVNLTTIASWLSWLQYFSIPRYGFTALQHNEFLGQNFCPGLNATGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 NPCNYATCTGEEYLVKQGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
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Search completed: September 18, 2008, 21:59:59
Job time : 234 secs

SCORE 3.0